

SEQUENCE LISTING

<110> Bayer HealthCare AG

<120> Diagnostics and Therapeutics for Diseases Associated with
Glycogen Synthase Kinase 3 beta (GSK3B)

<130> BHC 04 01 040

<160> 5

<170> PatentIn version 3.2

<210> 1

<211> 1639

<212> DNA

<213> Homo sapiens

<400> 1

atcatctata	tgttaaatat	ccgtgcccgt	ctgtcttgaa	ggagaaaatat	atcgcttgg	60
ttgtttttta	tagtatacaa	aaggagtgaa	aagccaaagag	gacgaagtct	ttttcttttt	120
cttcgtggg	agaacttaat	gctgcattta	tcgttaacct	aacaccccaa	cataaaagaca	180
aaaggaagaa	aaggaggaag	gaaggaaaag	gtgattcgcg	aagagagtga	tcatgtcagg	240
gcggcccaga	accacccct	ttgcggagag	ctgcaagccg	gtgcagcagc	cttcagctt	300
tggcagcatg	aaagtttagca	gagacaagga	cggcagcaag	gtgacaacag	tggtgtccaac	360
tcctggcag	ggtccagaca	gcccacaaga	agtcagctat	acagacacta	aagtgttgg	420
aaatggatca	tttgggtgtgg	tatataaagc	caaactttgt	gattcaggag	aactggtcgc	480
catcaagaaa	gtattgcagg	acaagagatt	taagaatcga	gagctccaga	tcatgagaaa	540
gctagatcac	tgtAACATAG	tccgattcg	ttatTTCTTC	tactccagtg	gtgagaagaa	600
agatgagggtc	tatctaatac	tggtgctgg	ctatgtccg	gaaacagtat	acagaggttc	660
cagacactat	agtcgagcca	aacagacgct	ccctgtgatt	tatgtcaagt	tgtatatagt	720
tca	cgatgttc	cgaagtttag	cctatatcca	ttcctttgg	atctgccatc	780
accgcagaac	ctcttgttgg	atctgtatac	tgctgtatta	aaactctgt	actttggaaag	840
tgcaaagca	ctggccgag	gagaacccaa	tgtttcgtat	atctgttctc	ggtactatag	900
ggcaccagag	ttgatctttg	gagccactga	ttatacctct	agtatagatg	tatggctcgc	960
tggctgtgt	ttggctgagc	tgttacttagg	acaaccaata	tttccagggg	atagtgtgt	1020
ggatcagttg	gtagaaataa	tcaaggtcct	gggaactcca	acaagggagc	aaatcagaga	1080
aatgaaccca	aactacacag	aatttaaatt	ccctcaaatt	aaggcacatc	cttggactaa	1140
ggattcgtca	ggaacaggac	atttcacctc	aggagtgcgg	gtcttccgac	cccgaactcc	1200
accggaggca	attgcactgt	gtagccgtct	gctggagtat	acaccaactg	cccgactaac	1260
accactggaa	gcttgcac	attcattttt	tgtgaatta	cgggacccaa	atgtcaaact	1320
acccaaatggg	cgagacacac	ctgcactt	caacttcacc	actcaagaac	tgtcaagtaa	1380
tccacccctg	gctaccatcc	ttatccctcc	tcatgtcgg	attcaagcag	ctgcttcaac	1440
ccccacaaat	gccacagcag	cgtcagatgc	taatactgg	gaccgtggac	agaccaataa	1500
tgctgtttct	gcatcagttt	ccaactccac	ctgaacagtc	ccgagcagcc	agctgcacag	1560

gaaaaaccac cagttacttg agtgtcactc agcaacactg gtcacgtttg gaaagaatat 1620
taaaaaaaaaaaa aaaaaaaaaa 1639

<210> 2

<211> 433

<212> PRT

<213> Homo sapiens

<400> 2

Met Ser Gly Arg Pro Arg Thr Thr Ser Phe Ala Glu Ser Cys Lys Pro

1 5 10 15

Val Gln Gln Pro Ser Ala Phe Gly Ser Met Lys Val Ser Arg Asp Lys

20 25 30

Asp Gly Ser Lys Val Thr Thr Val Val Ala Thr Pro Gly Gln Gly Pro

35 40 45

Asp Arg Pro Gln Glu Val Ser Tyr Thr Asp Thr Lys Val Ile Gly Asn

50 55 60

Gly Ser Phe Gly Val Val Tyr Gln Ala Lys Leu Cys Asp Ser Gly Glu

65 70 75 80

Leu Val Ala Ile Lys Lys Val Leu Gln Asp Lys Arg Phe Lys Asn Arg

85 90 95

Glu Leu Gln Ile Met Arg Lys Leu Asp His Cys Asn Ile Val Arg Leu

100 105 110

Arg Tyr Phe Phe Tyr Ser Ser Gly Glu Lys Lys Asp Glu Val Tyr Leu

115 120 125

Asn Leu Val Leu Asp Tyr Val Pro Glu Thr Val Tyr Arg Val Ala Arg

130 135 140

His Tyr Ser Arg Ala Lys Gln Thr Leu Pro Val Ile Tyr Val Lys Leu

145 150 155 160

Tyr Met Tyr Gln Leu Phe Arg Ser Leu Ala Tyr Ile His Ser Phe Gly

165 170 175

Ile Cys His Arg Asp Ile Lys Pro Gln Asn Leu Leu Asp Pro Asp

180 185 190

Thr Ala Val Leu Lys Leu Cys Asp Phe Gly Ser Ala Lys Gln Leu Val

195 200 205

Arg Gly Glu Pro Asn Val Ser Tyr Ile Cys Ser Arg Tyr Tyr Arg Ala

210 215 220

Pro Glu Leu Ile Phe Gly Ala Thr Asp Tyr Thr Ser Ser Ile Asp Val

225 230 235 240

Trp Ser Ala Gly Cys Val Leu Ala Glu Leu Leu Gly Gln Pro Ile

245 250 255

Phe Pro Gly Asp Ser Gly Val Asp Gln Leu Val Glu Ile Ile Lys Val

260 265 270

Leu Gly Thr Pro Thr Arg Glu Gln Ile Arg Glu Met Asn Pro Asn Tyr

275 280 285

Thr Glu Phe Lys Phe Pro Gln Ile Lys Ala His Pro Trp Thr Lys Asp
290 295 300
Ser Ser Gly Thr Gly His Phe Thr Ser Gly Val Arg Val Phe Arg Pro
305 310 315 320
Arg Thr Pro Pro Glu Ala Ile Ala Leu Cys Ser Arg Leu Leu Glu Tyr
325 330 335
Thr Pro Thr Ala Arg Leu Thr Pro Leu Glu Ala Cys Ala His Ser Phe
340 345 350
Phe Asp Glu Leu Arg Asp Pro Asn Val Lys Leu Pro Asn Gly Arg Asp
355 360 365
Thr Pro Ala Leu Phe Asn Phe Thr Thr Gln Glu Leu Ser Ser Asn Pro
370 375 380
Pro Leu Ala Thr Ile Leu Ile Pro Pro His Ala Arg Ile Gln Ala Ala
385 390 395 400
Ala Ser Thr Pro Thr Asn Ala Thr Ala Ala Ser Asp Ala Asn Thr Gly
405 410 415
Asp Arg Gly Gln Thr Asn Asn Ala Ala Ser Ala Ser Ala Ser Asn Ser
420 425 430
Thr

<210> 3
<211> 20
<212> DNA
<213> artificial sequence

<220>
<223> forward primer

<400> 3
ttccagggga tagtgtgtg 20

<210> 4
<211> 20
<212> DNA
<213> artificial sequence

<220>
<223> reverse primer

<400> 4
tttgctccct tgttggagtt 20

<210> 5
<211> 30

<212> DNA

<213> artificial sequence

<220>

<223> probe

<400> 5

tcagttggta gaaataatca aggtcctggg

30